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TECH CENTER 1600/2900

- 1 -

SEQUENCE LISTING



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JONES, Stacey A.
WILLSON, Timothy M.

<120> AN ORPHAN NUCLEAR RECEPTOR

<130> PU3474US2

<140> 09/276,935

<141> 1999-03-26

<150> 60/079,593

<151> 1998-03-27

<160> 18

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<213> Artificial Sequence

<220>

<223> Probe

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<211> 34

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<213> Artificial Sequence

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<210> 9
<211> 32
<212> DNA
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<220>
<223> Probe

<400> 9
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<210> 10
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<400> 10
Met Lys Lys Gly His His His His His Gly
1 5 10

<210> 11
<211> 316
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein

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20 25 30
Ile Arg Glu Leu Met Asp Ala Gln Met Lys Thr Phe Asp Thr Thr Phe
35 40 45
Ser His Phe Lys Asn Phe Arg Leu Pro Gly Val Leu Ser Ser Gly Cys
50 55 60
Glu Leu Pro Glu Ser Leu Gln Ala Pro Ser Arg Glu Glu Ala Ala Lys
65 70 75 80
Trp Ser Gln Val Arg Lys Asp Leu Cys Ser Leu Lys Val Ser Leu Gln
85 90 95
Leu Arg Gly Glu Asp Gly Ser Val Trp Asn Tyr Lys Pro Pro Ala Asp
100 105 110
Ser Gly Gly Lys Glu Ile Phe Ser Leu Leu Pro His Met Ala Asp Met
115 120 125

Ser Thr Tyr Met Phe Lys Gly Ile Ile Ser Phe Ala Lys Val Ile Ser
130 135 140
Tyr Phe Arg Asp Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu Lys Gly
145 150 155 160
Ala Ala Phe Glu Leu Cys Gln Leu Arg Phe Asn Thr Val Phe Asn Ala
165 170 175
Glu Thr Gly Thr Trp Glu Cys Gly Arg Leu Ser Tyr Cys Leu Glu Asp
180 185 190
Thr Ala Gly Gly Phe Gln Gln Leu Leu Leu Glu Pro Met Leu Lys Phe
195 200 205
His Tyr Met Leu Lys Lys Leu Gln Leu His Glu Glu Glu Tyr Val Leu
210 215 220
Met Gln Ala Ile Ser Leu Phe Ser Pro Asp Arg Pro Gly Val Leu Gln
225 230 235 240
His Arg Val Val Asp Gln Leu Gln Glu Gln Phe Ala Ile Thr Leu Lys
245 250 255
Ser Tyr Ile Glu Cys Asn Arg Pro Gln Pro Ala His Arg Phe Leu Phe
260 265 270
Leu Lys Ile Met Ala Met Leu Thr Glu Leu Arg Ser Ile Asn Ala Gln
275 280 285
His Thr Gln Arg Leu Leu Arg Ile Gln Asp Ile His Pro Phe Ala Thr
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<210> 12
<211> 242
<212> PRT
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<220>
<223> Protein

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Asn Met Gly Leu Asn Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile
35 40 45
Cys Gln Ala Ala Asp Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys
50 55 60
Arg Ile Pro His Phe Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu
65 70 75 80
Leu Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg
85 90 95
Ser Ile Ala Val Lys Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val
100 105 110
His Arg Asn Ser Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg
115 120 125
Val Leu Thr Glu Leu Val Ser Lys Met Arg Asp Met Gln Met Asp Lys
130 135 140

Thr Glu Leu Gly Cys Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser
145 150 155 160
Lys Gly Leu Ser Asn Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val
165 170 175
Tyr Ala Ser Leu Glu Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro
180 185 190
Gly Arg Phe Ala Lys Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile
195 200 205
Gly Leu Lys Cys Leu Glu His Leu Phe Phe Lys Leu Ile Gly Asp
210 215 220
Thr Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu Ala Pro His Gln
225 230 235 240
Met Thr

<210> 13
<211> 2146
<212> DNA
<213> Artificial Sequence

<220>
<223> Probe

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aagtgttac acgtgagaaaaa gcaagagaat aagctaatac tcctgtcctg aacaaggcag 180
cggttccttgc taaagctac tccttgatcg atcccttgc ccggattgtt caaagtggac 240
cccaggggag a aatcgagac aaagaactta ccaccaagca gtccaagagg cccagaagca 300
aacctggagg tgagacccaa agaaagctgg aaccatgctg actttgtaca ctgtgaggac 360
acagagtctg ttcttgaaa gcccagtgt aacgcagatg aggaagtctgg aggtccccaa 420
atctgcgtg tatgtgggg a caaggccact ggctatcact tcaatgtcat gacatgtgaa 480
ggatgcagg gcttttcag gagggccatg a aacgcacacg cccggctgag gtggcccttc 540
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cgcaagtgcc tggagagccg catgaagaag gatgatca tgtccgacga ggccgtggag 660
gagaggccgg ctttgcataa gccaagaaa agtgaacggc caggactca gccactggg 720
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ggcagtgtct ggaactacaa acccccagcc gacagtggcg gggaaagatc tttctccctg 1020
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gtcatctcct acttcaggga ctggcccatc gaggaccaga tctccctgc gaaaaaggcc 1140
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gagttgtggcc ggctgtccta ctgcttggaa gacactgcag gggcttcca gcaacttcta 1260
ctggagccca tgctgaaatt ccactacatg ctgaagaagc tgtagctgc tgaggaggag 1320
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cgcgtgggtt accagctgcg ggagcaattc gcaattactc tgaatcccta cattgaatgc 1440
aatcgcccccc agcctgctca taggttcttgc ttctgttgc a tcatggat gctcaccgag 1500
ctccgcagca tcaatgctca gcacacccag cgctgctgc gcatccaggaa catacacc 1560
tttgcacgc ccctcatgcg ggagttgttc ggcattcacag gtagctgagc ggctgccc 1620
gggtgacacc tccgagagggc agccagaccc agagccctct gaggccac tccggggcca 1680

agacagatgg acactgccaa gagccgacaa tgccctgctg gcctgtctcc ctaggaaatt 1740
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aggaccatca gagaggcaag gttgccctt cctttaaaaa ggccctgtgg tctggggaga 1920
aatccctcag atcccactaa agtgtcaagg tttggaaagg accaagcgac caaggatagg 1980
ccatctgggg tctatgccc catacccacg tttgttcgt tcctgagtct tttcattgct 2040
acctctaata gtcctgtctc ccacttccc ctgcgtcccc tcctcttccg agctgctttg 2100
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<210> 14

<211> 434

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein

<400> 14

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Glu Glu Val Gly Gly Pro Gln Ile Cys Arg Val Cys Gly Asp Lys Ala
35 40 45
Thr Gly Tyr His Phe Asn Val Met Thr Cys Glu Gly Cys Lys Gly Phe
50 55 60
Phe Arg Arg Ala Met Lys Arg Asn Ala Arg Leu Arg Cys Pro Phe Arg
65 70 75 80
Lys Gly Ala Cys Glu Ile Thr Arg Lys Thr Arg Arg Gln Cys Gln Ala
85 90 95
Cys Arg Leu Arg Lys Cys Leu Glu Ser Gly Met Lys Lys Glu Met Ile
100 105 110
Met Ser Asp Glu Ala Val Glu Glu Arg Arg Ala Leu Ile Lys Arg Lys
115 120 125
Lys Ser Glu Arg Thr Gly Thr Gln Pro Leu Gly Val Gln Gly Leu Thr
130 135 140
Glu Glu Gln Arg Met Met Ile Arg Glu Leu Met Asp Ala Gln Met Lys
145 150 155 160
Thr Phe Asp Thr Thr Phe Ser His Phe Lys Asn Phe Arg Leu Pro Gly
165 170 175
Val Leu Ser Ser Gly Cys Glu Leu Pro Glu Ser Leu Gln Ala Pro Ser
180 185 190
Arg Glu Glu Ala Ala Lys Trp Ser Gln Val Arg Lys Asp Leu Cys Ser
195 200 205
Leu Lys Val Ser Leu Gln Leu Arg Gly Glu Asp Gly Ser Val Trp Asn
210 215 220
Tyr Lys Pro Pro Ala Asp Ser Gly Gly Lys Glu Ile Phe Ser Leu Leu
225 230 235 240
Pro His Met Ala Asp Met Ser Thr Tyr Met Phe Lys Gly Ile Ile Ser
245 250 255
Phe Ala Lys Val Ile Ser Tyr Phe Arg Asp Leu Pro Ile Glu Asp Gln
260 265 270
Ile Ser Leu Leu Lys Gly Ala Ala Phe Glu Leu Cys Gln Leu Arg Phe

275 280 285
Asn Thr Val Phe Asn Ala Glu Thr Gly Thr Trp Glu Cys Gly Arg Leu
290 295 300
Ser Tyr Cys Leu Glu Asp Thr Ala Gly Gly Phe Gln Gln Leu Leu Leu
305 310 315 320
Glu Pro Met Leu Lys Phe His Tyr Met Leu Lys Lys Leu Gln Leu His
325 330 335
Glu Glu Glu Tyr Val Leu Met Gln Ala Ile Ser Leu Phe Ser Pro Asp
340 345 350
Arg Pro Gly Val Leu Gln His Arg Val Val Asp Gln Leu Gln Glu Gln
355 360 365
Phe Ala Ile Thr Leu Lys Ser Tyr Ile Glu Cys Asn Arg Pro Gln Pro
370 375 380
Ala His Arg Phe Leu Phe Leu Lys Ile Met Ala Met Leu Thr Glu Leu
385 390 395 400
Arg Ser Ile Asn Ala Gln His Thr Gln Arg Leu Leu Arg Ile Gln Asp
405 410 415
Ile His Pro Phe Ala Thr Pro Leu Met Gln Glu Leu Phe Gly Ile Thr
420 425 430
Gly Ser

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Probe

<400> 15
atatgaactc aaaggaggtc agtg

24

Sue D. West
<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Probe

<400> 16
atatgttctc aaaggagaac agtg

24

<210> 17
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<212> DNA
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<220>
<223> Probe

<400> 17
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24

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Probe

<400> 18
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21